

REV 0
1109

#2

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/976,605

DATE: 11/01/2001

TIME: 07:53:49

Input Set : A:\50082.015002.SEQLIST.TXT

Output Set: N:\CRF3\11012001\I976605.raw

4 <110> APPLICANT: MCFADDEN, GRANT
5 ESSANI, KARIM
7 <120> TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND POLYPEPTIDES
8 FOR IMMUNE MODULATION
12 <130> FILE REFERENCE: 50082/015002
C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/976,605 OK
C--> 14 <141> CURRENT FILING DATE: 2001-10-11

14 <150> PRIOR APPLICATION NUMBER: US 60/239,354
15 <151> PRIOR FILING DATE: 2000-10-11
17 <160> NUMBER OF SEQ ID NOS: 9
19 <170> SOFTWARE: FastSEQ for Windows Version 4.0

ENTERED

21 <210> SEQ ID NO: 1
22 <211> LENGTH: 26
23 <212> TYPE: PRT
24 <213> ORGANISM: Tanapox virus
26 <400> SEQUENCE: 1

27 Ile Thr Leu Lys Tyr Cys Tyr Thr Val Thr Leu Lys Asp Asn Gly Leu
28 1 5 10 15
29 Tyr Asp Lys Val Phe Tyr Cys His Tyr Asn
30 20 25

33 <210> SEQ ID NO: 2
34 <211> LENGTH: 338
35 <212> TYPE: PRT
36 <213> ORGANISM: Yaba Monkey tumor virus
38 <400> SEQUENCE: 2

39 Met Asn Lys Leu Ile Leu Phe Ser Thr Ile Val Ala Val Cys Asn Cys
40 1 5 10 15

41 Ile Thr Leu Lys Tyr Asn Tyr Thr Val Thr Leu Lys Asp Asn Gly Leu
42 20 25 30

43 Tyr Asp Gly Val Phe Tyr Asp His Tyr Asn Asp Gln Leu Val Thr Lys
44 35 40 45

45 Ile Ser Tyr Asn His Glu Thr Arg His Gly Asn Val Asn Phe Arg Ala
46 50 55 60

47 Asp Trp Phe Lys Ile Ser Arg Ser Pro His Thr Pro Gly Asn Asp Tyr
48 65 70 75 80

49 Asn Phe Asn Phe Trp Tyr Ser Leu Met Lys Glu Thr Leu Glu Glu Ile
50 85 90 95

51 Asn Lys Asn Asp Ser Thr Lys Thr Thr Ser Leu Ser Leu Ile Thr Gly
52 100 105 110

53 Cys Tyr Glu Thr Gly Leu Leu Phe Gly Ser Tyr Gly Tyr Val Glu Thr
54 115 120 125

55 Ala Asn Gly Pro Leu Ala Arg Tyr His Thr Gly Asp Lys Arg Phe Thr
56 130 135 140

57 Lys Met Thr His Lys Gly Phe Pro Lys Val Gly Met Leu Thr Val Lys
58 145 150 155 160

59 Asn Thr Leu Trp Lys Asp Val Lys Thr Tyr Leu Gly Gly Phe Glu Tyr
60 165 170 175

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61 Met Gly Cys Ser Leu Ala Ile Leu Asp Tyr Gln Lys Met Ala Lys Gly
62          180          185          190
63 Glu Ile Pro Lys Asp Thr Thr Pro Thr Val Lys Val Thr Gly Asn Glu
64          195          200          205
65 Leu Glu Asp Gly Asn Met Thr Leu Glu Cys Ser Val Asn Ser Phe Tyr
66          210          215          220
67 Pro Pro Asp Val Ile Thr Lys Trp Ile Glu Ser Glu His Phe Lys Gly
68 225          230          235          240
69 Glu Tyr Lys Tyr Val Asn Gly Arg Tyr Tyr Pro Glu Trp Gly Arg Lys
70          245          250          255
71 Ser Asp Tyr Glu Pro Gly Glu Pro Gly Phe Pro Trp Asn Ile Lys Lys
72          260          265          270
73 Asp Lys Asp Ala Asn Thr Tyr Ser Leu Thr Asp Leu Val Arg Thr Thr
74          275          280          285
75 Ser Lys Met Ser Ser Gln Leu Val Cys Val Val Phe His Asp Thr Leu
76          290          295          300
77 Glu Ala Gln Val Tyr Thr Cys Ser Glu Gly Cys Asn Gly Glu Leu Tyr
78 305          310          315          320
79 Asp His Leu Tyr Arg Lys Thr Glu Glu Gly Glu Gly Glu Glu Asp Glu
80          325          330          335
81 Glu Asp
85 <210> SEQ ID NO: 3
86 <211> LENGTH: 1183
87 <212> TYPE: DNA
88 <213> ORGANISM: Yaba Monkey tumor virus
90 <400> SEQUENCE: 3
91 atgaataagt taattttatc gttgttgggt tttgtggcaa cttgcaattg tataacctta 60
92 agatataatt ataccgttac ggtaaagaat ggattatacg acgggggtatt ttttgattat 120
93 tacaacgatac agtttagtaac gaggatatca tataaccatg aaactagaca cggaacgta 180
94 aattctagag cttcatggtt tgatatctct aaaagccctc atactccggg tgacgattac 240
95 cactttaact tttggtaccc gttaatgaaa gatactttgg agtccatcaa tagtaataaa 300
96 aacgaaagcg ataaatgttc ttcggtgtcg ttaattttgg ggtgttatga aacgggatct 360
97 ctttttggga gttacggata cgttgagtca agtggcggac cgttggctag gtatagcacg 420
98 aaagataaaa agtttttaaa aatgacagat aaaggatttc caaaggttgg aatgttaacc 480
99 gttcatggtc ctagttggca aacagttaaa aaatacgtgg gagggtttgt gtacgctgga 540
100 tgtttgc tag ctatttttga ttatcaaaaa atggctaaga ataacatacc tagtaatgta 600
101 atgccaaactg ttacggtaaac ggggtgaggaa ctgcaagatg gtaacacaac gcttaagtgt 660
102 aacgtaaaat ctttttaccc tccagacgta atgatcaagt ggatagaaag taaatatttt 720
103 aacggtgaat atagatacgt taatggaaga gaatacccg aatggggaag gcaatcagat 780
104 tatgagccc gagagccagg ttttcggtta catccaaaaa aagatgacgg taaaaccact 840
105 tacagccttt tagatttttg tcgcactacg tcaggattaa ctagtcagtt agtttgtgtt 900
106 gttttccatg acacgtttga atcgagggtt aatacatggt ccgaagggtg tgaaggtaaa 960
107 ttatacgatc acctatatag aaaatcggaa gaaggagacg aggttgtgga ggacgaagaa 1020
108 gactgaaaac aagtcgtggt ggaagctggt ctgatcgcgc gtttacgttt ccgctagacg 1080
109 gaagtttgcc gcccgagagg gcgatgtttt ttttaaaaaa tgaaaaagta gatgataccg 1140
110 agcgatgacc gcgaaatgga gggtattaca gacggcgtgt tcg 1183
112 <210> SEQ ID NO: 4
113 <211> LENGTH: 338
114 <212> TYPE: PRT

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115 <213> ORGANISM: Tanapox virus
117 <400> SEQUENCE: 4
118 Met Asn Lys Leu Ile Leu Phe Ser Thr Ile Val Ala Val Cys Asn Cys
119 1 5 10 15
120 Ile Thr Leu Lys Tyr Asn Tyr Thr Val Thr Leu Lys Asp Asn Gly Leu
121 20 25 30
122 Tyr Asp Gly Val Phe Tyr Asp His Tyr Asn Asp Gln Leu Val Thr Lys
123 35 40 45
124 Ile Ser Tyr Asn His Glu Thr Arg His Gly Asn Val Asn Phe Arg Ala
125 50 55 60
126 Asp Trp Phe Lys Ile Ser Arg Ser Pro His Thr Pro Gly Asn Asp Tyr
127 65 70 75 80
128 Asn Phe Asn Phe Trp Tyr Ser Leu Met Lys Glu Thr Leu Glu Glu Ile
129 85 90 95
130 Asn Lys Asn Asp Ser Thr Lys Thr Thr Ser Leu Ser Leu Ile Thr Gly
131 100 105 110
132 Cys Tyr Glu Thr Gly Leu Leu Phe Gly Ser Tyr Gly Tyr Val Glu Thr
133 115 120 125
134 Ala Asn Gly Pro Leu Ala Arg Tyr His Thr Gly Asp Lys Arg Phe Thr
135 130 135 140
136 Lys Met Thr His Lys Gly Phe Pro Lys Val Gly Met Leu Thr Val Lys
137 145 150 155 160
138 Asn Thr Leu Trp Lys Asp Val Lys Thr Tyr Leu Gly Gly Phe Glu Tyr
139 165 170 175
140 Met Gly Cys Ser Leu Ala Ile Leu Asp Tyr Gln Lys Met Ala Lys Gly
141 180 185 190
142 Glu Ile Pro Lys Asp Thr Thr Pro Thr Val Lys Val Thr Gly Asn Glu
143 195 200 205
144 Leu Glu Asp Gly Asn Met Thr Leu Glu Cys Ser Val Asn Ser Phe Tyr
145 210 215 220
146 Pro Pro Asp Val Ile Thr Lys Trp Ile Glu Ser Glu His Phe Lys Gly
147 225 230 235 240
148 Glu Tyr Lys Tyr Val Asn Gly Arg Tyr Tyr Pro Glu Trp Gly Arg Lys
149 245 250 255
150 Ser Asp Tyr Glu Pro Gly Glu Pro Gly Phe Pro Trp Asn Ile Lys Lys
151 260 265 270
152 Asp Lys Asp Ala Asn Thr Tyr Ser Leu Thr Asp Leu Val Arg Thr Thr
153 275 280 285
154 Ser Lys Met Ser Ser Gln Leu Val Cys Val Val Phe His Asp Thr Leu
155 290 295 300
156 Glu Ala Gln Val Tyr Thr Cys Ser Glu Gly Cys Asn Gly Glu Leu Tyr
157 305 310 315 320
158 Asp His Leu Tyr Arg Lys Thr Glu Glu Gly Glu Gly Glu Glu Asp Glu
159 325 330 335
160 Glu Asp
164 <210> SEQ ID NO: 5
165 <211> LENGTH: 1034
166 <212> TYPE: DNA
167 <213> ORGANISM: Tanapox virus

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Input Set : A:\50082.015002.SEQLIST.TXT

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169 <400> SEQUENCE: 5

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170 aagcttcattg aataagttaa tattatttag cacaattgta gcagtttgta actgcataac 60
171 tttaaaaatat aattatactg ttacgttaaa agataatggg ttatacgatg gagtatttta 120
172 cgatcattac aacgatcagt tagtaacgaa aatatcatat aaccacgaaa ctagacacgg 180
173 aaacgtaaat tttagggtcg attgggttaa tttttctagg agtccccaca cgccaggtaa 240
174 cgattacaac ttttaactttt ggtattcttt aatgaaagaa actttagaag aaattaataa 300
175 aaacgatagc acaaaaaacta cttcgctttc attaatcact ggggtgttatg aaacaggatt 360
176 attatttggt agttatgggt atgtagaaac ggccaacgga ccgttgcca gataccatac 420
177 aggagataaa aggtttacga aaatgacaca taaaggtttt cccaagggtg gaatgttaac 480
178 tgtaaaaaac actctttgga aagatgtaaa aacttatcta ggcggttttg aatacatggg 540
179 atgttcatta gctatttttag attaccaaaa aatggctaaa ggtgaaatac caaagatac 600
180 aacacctaca gtgaaagtaa cgggtaatga gttagaagat ggtaacatga ctcttgaatg 660
181 cagtgtaaat tcattttacc ctctgacgt aattactaag tggatagaaa gcgaacattt 720
182 taaaggtgaa tataaatatg ttaacggaag atactatcca gaatggggga gaaaatccga 780
183 ttatgagcca ggagagccag gttttccatg gaattattaaa aaagataaag atgcaaacac 840
184 atatagttaa acagatttag tacgtacaac atcaaaaatg agtagtcaac tagtatgtgt 900
185 tgttttccat gacacttttag aagcgcaagt ttatacttgt tctgaaggat gcaatggaga 960
186 gctatacgac cacctatata gaaaaacaga agaaggagaa ggtgaagagg atgaagaaga 1020
187 cggaaccct cgag                                     1034

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189 <210> SEQ ID NO: 6

190 <211> LENGTH: 338

191 <212> TYPE: PRT

192 <213> ORGANISM: Yaba-like disease virus

194 <400> SEQUENCE: 6

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195 Met Asp Lys Leu Leu Leu Phe Ser Thr Ile Val Ala Val Cys Asn Cys
196 1 5 10 15
197 Ile Thr Leu Lys Tyr Asn Tyr Thr Val Thr Leu Lys Asp Asp Gly Leu
198 20 25 30
199 Tyr Asp Gly Val Phe Tyr Asp His Tyr Asn Asp Gln Leu Val Thr Lys
200 35 40 45
201 Ile Ser Tyr Asn His Glu Thr Arg His Gly Asn Val Asn Phe Arg Ala
202 50 55 60
203 Asp Trp Phe Asn Ile Ser Arg Ser Pro His Thr Pro Gly Asn Asp Tyr
204 65 70 75 80
205 Asn Phe Asn Phe Trp Tyr Ser Leu Met Lys Glu Thr Leu Glu Glu Ile
206 85 90 95
207 Asn Lys Asn Asp Ser Thr Lys Thr Thr Ser Leu Ser Leu Ile Thr Gly
208 100 105 110
209 Cys Tyr Glu Thr Gly Leu Leu Phe Gly Ser Tyr Gly Tyr Val Glu Thr
210 115 120 125
211 Ala Asn Gly Pro Leu Ala Arg Tyr His Thr Gly Asp Lys Arg Phe Thr
212 130 135 140
213 Lys Met Thr His Lys Gly Phe Pro Lys Val Gly Met Leu Thr Val Lys
214 145 150 155 160
215 Asn Thr Leu Trp Lys Asp Val Lys Ala Tyr Leu Gly Gly Phe Glu Tyr
216 165 170 175
217 Met Gly Cys Ser Leu Ala Ile Leu Asp Tyr Gln Lys Met Ala Lys Gly
218 180 185 190
219 Lys Ile Pro Lys Asp Thr Thr Pro Thr Val Lys Val Thr Gly Asn Glu

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220          195          200          205
221 Leu Glu Asp Gly Asn Met Thr Leu Glu Cys Thr Val Asn Ser Phe Tyr
222          210          215          220
223 Pro Pro Asp Val Ile Thr Lys Trp Ile Glu Ser Glu His Phe Lys Gly
224 225          230          235          240
225 Glu Tyr Lys Tyr Val Asn Gly Arg Tyr Tyr Pro Glu Trp Gly Arg Lys
226          245          250          255
227 Ser Asn Tyr Glu Pro Gly Glu Pro Gly Phe Pro Trp Asn Ile Lys Lys
228          260          265          270
229 Asp Lys Asp Ala Asn Thr Tyr Ser Leu Thr Asp Leu Val Arg Thr Thr
230          275          280          285
231 Ser Lys Met Ser Ser Gln Pro Val Cys Val Val Phe His Asp Thr Leu
232          290          295          300
233 Glu Ala Gln Val Tyr Thr Cys Ser Glu Gly Cys Asn Gly Glu Leu Tyr
234 305          310          315          320
235 Asp His Leu Tyr Arg Lys Thr Glu Glu Gly Glu Gly Glu Glu Asp Glu
236          325          330          335
237 Glu Asp
241 <210> SEQ ID NO: 7
242 <211> LENGTH: 1017
243 <212> TYPE: DNA
244 <213> ORGANISM: Yaba-like disease virus
246 <400> SEQUENCE: 7
247 atggataagt tactattatt tagcacaatt gtagcagttt gtaactgcat aactttaaaa 60
248 tataattata ctgttacgtt aaaagatgat gggttatacg atggagtatt ttacgatcat 120
249 tacaacgatac agtttagtgac gaaaatatca tataaccatg aaactagaca cggaaacgta 180
250 aatttttaggg ctgattgggtt taatatttct aggagtcccc acacgccagg taacgattat 240
251 aactttaact tttggtattc tttaatgaaa gaaacttttag aagaaattaa taaaaacgat 300
252 agcacaaaaa ctacttcgct ttcattaatc actgggtggt atgaaacagg attattattt 360
253 ggtagttatg ggtatgtaga aacggccaac gggccgttgg ccagatacca tacaggagat 420
254 aaaaggttta cgaatatgac acataaagggt tttcccaagg ttggaatgtt aactgtaaaa 480
255 aacactcttt ggaaagatgt aaaagcttat ttaggcggtt ttgaatatat gggatgttca 540
256 ttagctattt tagattacca aaaaatggct aaaggtaaaa taccaaaaga tacaacacct 600
257 acagtgaaag taacgggtaa tgagttagaa gatggtaaca tgactcttga atgcactgta 660
258 aattcatttt accctoctga cgtaattact aagtggatag aaagcgaaca ttttaaagggt 720
259 gaatataaat atgttaacgg aagatactat ccagaatggg ggagaaaatc caattatgag 780
260 ccaggagagc caggttttcc atggaatatc aaaaaagata aagatgcaaa tacatatagt 840
261 ttaacagatt tagtacgtac aacatcaaaa atgagtagtc aaccagtatg tgttgttttc 900
262 catgacactt tagaagcgca agttttact tgttctgaag gatgcaatgg agagctatac 960
263 gatcacctat atagaaaaac agaagaaggg gaaggtgaag aggatgaaga agactga 1017
265 <210> SEQ ID NO: 8
266 <211> LENGTH: 340
267 <212> TYPE: PRT
268 <213> ORGANISM: Swinepox virus (C1L)
270 <400> SEQUENCE: 8
271 Met Ile Thr Lys Ala Ile Val Ile Leu Ser Ile Ile Thr Ala Tyr Val
272 1          5          10          15
273 Asp Ala Ser Ala Phe Leu Val Tyr Asn Tyr Thr Tyr Thr Leu Gln Asp
274          20          25          30

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VERIFICATION SUMMARY

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Input Set : A:\50082.015002.SEQLIST.TXT

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L:14 M:270 C: Current Application Number differs, Replaced Current Application No

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date